

Andres

#18

Page 1 of 7

1646

ENTERED

RECEIVED

AUG 02 2000

TECH CENTER 1600/2900

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/394,020A DATE: 07/18/2000  
TIME: 13:52:13  
  
Input Set : A:\SeqLstg.txt  
Output Set: N:\CRF3\07182000\I394020A.raw  
  
SEQUENCE LISTING  
4 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: Pepicelli, Carmen V  
6 Lewis, Paula M  
7 McMahon, Andrew P  
10 (ii) TITLE OF INVENTION: Regulation of Lung Tissue by  
11 Hedgehog-like Polypeptides, and Formulations and Uses  
12 Related Thereto  
14 (iii) NUMBER OF SEQUENCES: 24  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: Foley, Hoag & Eliot, LLP  
18 (B) STREET: One Post Office Square  
19 (C) CITY: Boston  
20 (D) STATE: MA  
21 (E) COUNTRY: USA  
22 (F) ZIP: 02109  
24 (v) COMPUTER READABLE FORM:  
25 (A) MEDIUM TYPE: Floppy disk  
26 (B) COMPUTER: IBM PC compatible  
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
28 (D) SOFTWARE: ASCII(text)  
C--> 30 (vi) CURRENT APPLICATION DATA:  
C--> 31 (A) APPLICATION NUMBER: US/09/394,020A  
C--> 32 (B) FILING DATE: 10-Sep-1999  
33 (C) CLASSIFICATION:  
35 (vii) PRIOR APPLICATION DATA:  
36 (A) APPLICATION NUMBER: US 60/099,952  
C--> 37 (B) FILING DATE: 11-SEP-1998  
39 (viii) ATTORNEY/AGENT INFORMATION:  
40 (A) NAME: Vincent, Matthew P  
41 (B) REGISTRATION NUMBER: 36,709  
42 (C) REFERENCE/DOCKET NUMBER: HUV-032.01  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: (617) 832-1000  
46 (B) TELEFAX: (617) 832-7000  
48 (2) INFORMATION FOR SEQ ID NO: 1:  
49 (i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 1277 base pairs  
51 (B) TYPE: nucleic acid  
52 (C) STRANDEDNESS: both  
53 (D) TOPOLOGY: linear  
55 (ii) MOLECULE TYPE: cDNA  
57 (ix) FEATURE:  
58 (A) NAME/KEY: CDS  
59 (B) LOCATION: 1..1275  
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
63 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC

RAW SEQUENCE LISTING DATE: 07/18/2000  
 PATENT APPLICATION: US/09/394,020A TIME: 13:52:13

Input Set : A:\SeqLstg.txt  
 Output Set: N:\CRF3\07182000\I394020A.raw

64	Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
65	1 5 10 15	
67	TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC	96
68	Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
69	20 25 30	
71	ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG	144
72	Ile Gly Lys Arg Arg His Pro Lys Leu Thr Pro Leu Ala Tyr Lys	
73	35 40 45	
75	CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA	192
76	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	
77	50 55 60	
79	TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC	240
80	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	
81	65 70 75 80	
83	CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA	288
84	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly	
85	85 90 95	
87	GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG ATT GCC CTG	336
88	Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu	
89	100 105 110	
91	GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC	384
92	Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr	
93	115 120 125	
95	GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC	432
96	Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr	
97	130 135 140	
99	GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG	480
100	Glu Gly Arg Ala Val Asp Ile Thr Ser Asp Arg Asp Arg Ser Lys	
101	145 150 155 160	
103	TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC	528
104	Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
105	165 170 175	
107	TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC	576
108	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
109	180 185 190	
111	TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG	624
112	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
113	195 200 205	
115	CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG	672
116	His Leu Glu His Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
117	210 215 220	
119	GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC	720
120	Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
121	225 230 235 240	
123	TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC	768
124	Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
125	245 250 255	
127	GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC	816
128	Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Thr Ala Ala	

RAW SEQUENCE LISTING DATE: 07/18/2000  
 PATENT APPLICATION: US/09/394,020A TIME: 13:52:14

Input Set : A:\SeqLstg.txt  
 Output Set: N:\CRF3\07182000\I394020A.raw

129	260	265	270	
131	CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG			864
132	His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly			
133	275	280	285	
135	TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA			912 ~
136	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln			
137	290	295	300	
139	CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT			960
140	Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser			
141	305	310	315	320
143	GTC CAC AGC GTC TCA TTG CGG GAG GCG TCC GGA GCC TAC GCC CCA			1008
144	Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro			
145	325	330	335	
147	CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC			1056
148	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys			
149	340	345	350	
151	TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA			1104
152	Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro			
153	355	360	365	
155	TTC CGC TTG GCT CAG GGG CTG CTG GCC CTC TGC CCA GAT GGG GCC			1152
156	Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala			
157	370	375	380	
159	ATC CCT ACT GCC GCC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG			1200
160	Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg			
161	385	390	395	400
162	CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT			1248
163	Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His			
164	405	410	415	
166	CCG CTG GGC ATG GTG GCA CCG GCC AGC TG			1277
167	Pro Leu Gly Met Val Ala Pro Ala Ser			
168	420	425		
171	(2) INFORMATION FOR SEQ ID NO: 2:			
173	(i) SEQUENCE CHARACTERISTICS:			
174	(A) LENGTH: 1190 base pairs			
175	(B) TYPE: nucleic acid			
176	(C) STRANDEDNESS: both			
177	(D) TOPOLOGY: linear			
179	(ii) MOLECULE TYPE: cDNA			
181	(ix) FEATURE:			
182	(A) NAME/KEY: CDS			
183	(B) LOCATION: 1..1191			
185	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
187	ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG			48
188	Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu			
189	1	5	10	15
191	GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG			96
192	Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg			
193	20	25	30	
195	CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT			144

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/394,020A

DATE: 07/18/2000  
TIME: 13:52:14

Input Set : A:\SeqLstg.txt  
Output Set: N:\CRF3\07182000\I394020A.raw

196	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe	
197				35				40				45					192
199	GTC	CCC	AGT	ATG	CCC	GAG	CGG	ACC	CTG	GGC	GCG	AGT	GGG	CCA	GCG	GAG	
200	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
201				50				55			60						
203	GGG	AGG	GTA	ACA	AGG	GGG	TCG	GAG	CGG	TTC	CGG	GAC	CTC	GTA	CCC	AAC	240
204	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
205				65				70			75			80			
207	TAC	AAC	CCC	GAC	ATA	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGC	GGC	GCA	GAC	288
208	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
209				85				90			95						
211	CGC	CTG	ATG	ACA	GAG	CGT	TGC	AAA	GAG	CGG	GTG	AAC	GCT	CTA	GCC	ATC	336
212	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
213				100				105			110						
215	GCG	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTA	CGC	CTA	CGT	GTG	ACT	GAA	GGC	384
216	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
217				115				120			125						
219	TGG	GAC	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC		432
220	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
221				130				135			140						
223	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	480
224	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
225				145				150			155			160			
227	TTG	TGCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC		528
228	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
229				165				170			175						
231	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
232	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
233				180				185			190						
235	GCG	GTC	CGA	GCC	GGA	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	624
236	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
237				195				200			205						
239	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	672
240	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
241				210				215			220						
243	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GGC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	720
244	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
245				225				230			235			240			
247	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG	768
248	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
249				245				250			255						
251	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	816
252	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
253				260				265			270						
255	GTC	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	864
256	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
257				275				280			285						
259	GTC	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	
260	Val	Phe	Ala	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly		912

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/394,020A DATE: 07/18/2000  
TIME: 13:52:14

Input Set : A:\SeqLstg.txt  
Output Set: N:\CRF3\07182000\I394020A.raw

261	290	295	300			
263	GGG GAC GCG CTC CAG CCG CGC CGC GTA GCC CGC GTG GCG CGC GAG GAA			960		
264	Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu					
265	305	310	315	320		
267	GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC			1008		
268	Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val					
269	325	330	335			
271	AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG			1056		
272	Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp					
273	340	345	350			
275	GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT			1104		
276	Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala					
277	355	360	365			
279	CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT			1152		
280	Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser					
281	370	375	380			
283	CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG			1190		
284	Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly					
285	385	390	395			
288	(2) INFORMATION FOR SEQ ID NO: 3:					
290	(i) SEQUENCE CHARACTERISTICS:					
291	(A) LENGTH: 1281 base pairs					
292	(B) TYPE: nucleic acid					
293	(C) STRANDEDNESS: both					
294	(D) TOPOLOGY: linear					
296	(ii) MOLECULE TYPE: cDNA					
299	(ix) FEATURE:					
300	(A) NAME/KEY: CDS					
301	(B) LOCATION: 1..1233					
303	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:					
305	ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG			48		
306	Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu					
307	307 1	5	10	15		
309	CTG CTG CTG CTT CTG GTG CCG GCG CGG GGC TGC GGG CCG CGG CGG			96		
310	Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg					
311	20	25	30			
313	GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC			144		
314	Val Val Gly Ser Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala					
315	35	40	45			
317	TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC			192		
318	Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser					
319	50	55	60			
321	GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG			240		
322	Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu					
323	65	70	75	80		
325	CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC			288		
326	Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn					
327	85	90	95			
329	ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC			336		

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/394,020A

DATE: 07/18/2000  
TIME: 13:52:15

Input Set : A:\SeqLstg.txt  
Output Set: N:\CRF3\07182000\I394020A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:36 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:  
L:37 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:  
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:2287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2385 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23, Value=[not relevant]